

## RAW SEQUENCE LISTING

DATE: 08/02/2001

PATENT APPLICATION: US/09/834,722

TIME: 10:41:35

Input Set : A:\frwk3.ST25.txt

Output Set: N:\CRF3\08022001\I834722.raw

ENTERED

5 <110> APPLICANT: Farwick, Mike  
 7 Huthmacher, Klaus  
 9 Marx, Achim  
 11 Pfefferle, Walter  
 15 <120> TITLE OF INVENTION: New Nucleotide Sequences Which Code for the menE Gene  
 19 <130> FILE REFERENCE: 21123/280112  
 23 <140> CURRENT APPLICATION NUMBER: 09/834,722  
 25 <141> CURRENT FILING DATE: 2001-04-16  
 29 <160> NUMBER OF SEQ ID NOS: 4  
 33 <170> SOFTWARE: PatentIn version 3.0  
 37 <210> SEQ ID NO: 1  
 39 <211> LENGTH: 1570  
 41 <212> TYPE: DNA  
 43 <213> ORGANISM: Corynebacterium glutamicum  
 47 <220> FEATURE:  
 49 <221> NAME/KEY: CDS  
 51 <222> LOCATION: (230)..(1357)  
 55 <400> SEQUENCE: 1  
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 58 gtcaccaaca atggtttgga actcaccggc gcaatcggcg ctggcgcgct gcttctcatc 120  
 60 gcagttggcg caggtgcatg gagcatcgac ggggttcttg caaaacgcaa ggcctaaatc 180  
 62 tagcgcacaca actccgaatt ctgaaccatc ggcaactagaa tctcggaat atg aat act 238  
 63 Met Asn Thr  
 64 1  
 66 cgc gtc ctc gaa gca cta cct gtt gat ctt gca gat ccc acc gca att 286  
 67 Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro Thr Ala Ile  
 68 5 10 15  
 70 ctg gga gat ctc gag gac gca atc tct ggg aag aaa act ttc ctc ccc 334  
 71 Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr Phe Leu Pro  
 72 20 25 30 35  
 74 atc cct gta caa gat aaa acc cgt gca cag ttg ctg cgc gat tct caa 382  
 75 Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg Asp Ser Gln  
 76 40 45 50  
 78 cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc act 430  
 79 Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala Thr  
 80 55 60 65  
 82 tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg aat 478  
 83 Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu Asn  
 84 70 75 80  
 86 ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa ggc 526  
 87 Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu Gly  
 88 85 90 95  
 90 cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag gtg 574  
 91 Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln Val  
 92 100 105 110 115  
 94 ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat ctc 622  
 95 Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp Leu

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96          120          125          130
98 agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa ctg      670
99 Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu Leu
100          135          140          145
102 aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag tta      718
103 Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln Leu
104          150          155          160
106 ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt ttt      766
107 Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu Phe
108          165          170          175
110 gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga att      814
111 Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg Ile
112 180          185          190          195
114 tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc tca      862
115 Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser Ser
116          200          205          210
118 gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc gcg      910
119 Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly Ala
120          215          220          225
122 aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg att      958
123 Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met Ile
124          230          235          240
126 gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac gag      1006
127 Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn Glu
128          245          250          255
130 ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att ctc      1054
131 Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile Leu
132 260          265          270          275
134 acc gtg act ggt cgc gtg gat acc gtc att gat tcc ggt gga ttg aag      1102
135 Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly Gly Leu Lys
136          280          285          290
138 ttg cac cca gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc      1150
139 Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val
140          295          300          305
142 acc gcg gcg tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca      1198
143 Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala
144          310          315          320
146 att gtg gcc gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa      1246
147 Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu
148          325          330          335
150 ggc ctc gac gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat      1294
151 Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His
152 340          345          350          355
154 ctg gaa tct ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct      1342
155 Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala
156          360          365          370
158 atc gcg aag ctg ttt tagtcttcat tcttgctggc tgcaactagt tttgccacat      1397
159 Ile Ala Lys Leu Phe
160          375

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162 cttcatcggt gtacactttg gcgatctgct catcatttcc acccatgagg gtgttgccaa 1457
164 caactagtgc tcccacttgg gtgggtgggca cgacagcgaa gtgtcggggc tgagcgtaga 1517
166 cctggcgaat agggatgatca gacgcagtg cgcaggcatg cagccatacg tca 1570
169 <210> SEQ ID NO: 2
171 <211> LENGTH: 376
173 <212> TYPE: PRT
175 <213> ORGANISM: Corynebacterium glutamicum
179 <400> SEQUENCE: 2
181 Met Asn Thr Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro
182 1 5 10 15
185 Thr Ala Ile Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr
186 20 25 30
189 Phe Leu Pro Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg
190 35 40 45
193 Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val
194 50 55 60
197 Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr
198 65 70 75 80
201 Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly
202 85 90 95
205 Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly
206 100 105 110
209 Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala
210 115 120 125
213 Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala
214 130 135 140
217 Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro
218 145 150 155 160
221 Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu
222 165 170 175
225 Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln
226 180 185 190
229 Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr
230 195 200 205
233 Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile
234 210 215 220
237 Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly
238 225 230 235 240
241 Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe
242 245 250 255
245 Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp
246 260 265 270
249 Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly
250 275 280 285
253 Gly Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile
254 290 295 300
257 Lys Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu
258 305 310 315 320
261 Gly Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu

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```

262          325          330          335
265 Val Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg
266          340          345          350
269 Leu Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp
270          355          360          365
273 Arg Arg Ala Ile Ala Lys Leu Phe
274          370          375
277 <210> SEQ ID NO: 3
279 <211> LENGTH: 19
281 <212> TYPE: DNA
283 <213> ORGANISM: PCR primer
287 <400> SEQUENCE: 3
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291 <210> SEQ ID NO: 4
293 <211> LENGTH: 19
295 <212> TYPE: DNA
297 <213> ORGANISM: PCR primer
301 <400> SEQUENCE: 4
302 caggtgcatt tctgtagcc                                     19

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VERIFICATION SUMMARY

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